


```

QY 61 AINPDSSSEYRWYGESYVGRHPYKQFVAHDLRVNLLEGSRSYQVYCFNLKAFPLGSD 120
DB 61 AINPDSSSEYRWYGESYVGRHPYKQFVAHDLRVNLLEGSRSYQVYCFNLKAFPLGSD 120
QY 121 SSYKWKWKKHGDISTRKEDYAMSPTIGDNLKRLAVMTNGHPQANANGIMEGLEPINA1 180
DB 121 SSYKWKWKKHGDISTRKEDYAMSPTIGDNLKRLAVMTNGHPQANANGIMEGLEPINA1 180
QY 181 RYVQEAAMYSDNAPISNPDESFRSESNLVSTQSLMRQALCOLIDNLA1TKMPKQV 240
DB 181 RYVQEAAMYSDNAPISNPDESFRSESNLVSTQSLMRQALCOLIDNLA1TKMPKQV 240
QY 241 PDDPQUSIFESEDKGDKYKNGYONLSGLVPTKPTGDPMPMPNPQPTTSVYLIRRYAI 300
DB 241 PDDPQUSIFESEDKGDKYKNGYONLSGLVPTKPTGDPMPMPNPQPTTSVYLIRRYAI 300
QY 301 GDYSKLEGGATLDTGNNVNSFOARVSSNDIGERIELSDGTYTLTELSNPAGSIAP1 360
DB 301 GDYSKLEGGATLDTGNNVNSFOARVSSNDIGERIELSDGTYTLTELSNPAGSIAP1 360
QY 361 TFFVEAGKYVTIIDKQIENPKEIYEPYVEAYNDEFEFSVLTQNYAKFYAKKNGS 420
DB 361 TFFVEAGKYVTIIDKQIENPKEIYEPYVEAYNDEFEFSVLTQNYAKFYAKKNGS 420
QY 421 SQVYVCFNADLSPDSEDEGKTMTPTDFTTGKVKYTHIAGRDLFKYTVKPRDTPDPTFLK 480
DB 421 SQVYVCFNADLSPDSEDEGKTMTPTDFTTGKVKYTHIAGRDLFKYTVKPRDTPDPTFLK 480
QY 481 HIKKVEKGYREGQALEYSGLTETQARATQALAIYFTTSABELDKKLDYHGFQGMND 540
DB 481 HIKKVEKGYREGQALEYSGLTETQARATQALAIYFTTSABELDKKLDYHGFQGMND 540
QY 541 STLAVALKILEYADSNPQTLDTLDFEIPNNNKYQSLIGTQMPHEDLVDTIIRMEDKKEVI 600
DB 541 STLAVALKILEYADSNPQTLDTLDFEIPNNNKYQSLIGTQMPHEDLVDTIIRMEDKKEVI 600
QY 601 PVTNHLTLKRTVYGLAGDRKDPHFETELKNNKOEILSQTVKTDKTNLEFKDKGATINLK 660
DB 601 PVTNHLTLKRTVYGLAGDRKDPHFETELKNNKOEILSQTVKTDKTNLEFKDKGATINLK 660
QY 661 HGSGLTLQGLPEGYSYLVKRETSDEGKYKVNQSOEVANATVSKGITSDEFLAENNEPEV 720
DB 661 HGSGLTLQGLPEGYSYLVKRETSDEGKYKVNQSOEVANATVSKGITSDEFLAENNEPEV 720
QY 721 VPTGVQDKINGYALAIYAGISLGIWGIHTIRIRKHD 757
DB 721 VPTGVQDKINGYALAIYAGISLGIWGIHTIRIRKHD 757

RESULT 2
US-09-494-297-4
; Sequence 4, Application us/09494297
; GENERAL INFORMATION:
; APPLICANT: PODBIELSKI, ANDREAS
; TITLE OF INVENTION: COLLAGEN-BINDING PROTEINS FROM STREPTOCOCCUS PYOGENES
; FILE REFERENCE: P06628U0/SBS
; CURRENT APPLICATION NUMBER: US/09/494,297
; CURRENT FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
; US-09-494-297-4

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Query Match 49.6%; Score 1958.5; DB 18; Length 742;
Best Local Similarity 54.3%; Pred. No. 2e-156;
Matches 400; Conservative 116; Mismatches 196; Indels 25; Gaps 13;

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QY 20 SKNSKR--FTVTVGVFMIFALVTGAVGAKTYFGVLESTPAINPDSSSEYRWYGES 77
DB 11 SANNNRRQTTIGLTKVFLTFVALIGVGFIRAFGAEOQVNP--RQSSIQDYPWGYDS 68

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QY 78 YVNGHPYKQFVAHDLRVNLLEGSRSYQVYCFNLKAFPLGSDSYKWKYKHGDISTRK 137
DB 69 YPKGYDPYSPDKTYHNLKAVNLEGSKQYQALCFNLTKHFPKSDSVRSQWKKLEGNTENF 128
QY 138 EDYAMSPRTIGDELNOKRLAVMTNGHPQANANGIMEGLEPINA1RYVQEAAMYSDNAPIS 197
DB 129 IKLADKPRIEDQLOQNIILIRILYNGVYNNKGMIMKGDIPNALILVQNA1W-YTDSAQI- 186
QY 198 NPDESFRSESNLVSTQSLMRQALCOLIDNLA1TKMPKQVDDPQUSIFESEDKGDK 257
DB 187 NPDESFRSESNLVSTQSLMRQALCOLIDNLA1TKMPKQVDDPQUSIFESEDKGDK 257
QY 258 YNKGYNLSGLVPTKPTGDPMPMPNPQPTTSVYLIRRYAIGDYSKLEGGATLDTGSD 317
DB 243 --KPFQNLIAEYVDPDPKPGEE--PPATKTSVYLIRRYAGSD--SKLEGGATLKSQI 297
QY 318 NVNSFOARVSSNDIGERIELSDGTYTLTELSNPAGSIAP1PFFVEAGKYVTI-IDK 376
DB 298 EGSQFOEKDPQSNLSGTEVLPNGYTVLTETSSPDGKYKIAEP1KFRVKNKVFYVOKDGS 357
QY 377 QIENPKEIYEPYVEAYNDEFEFSVLT--TONYAKFYAKKNGSSQVYCFNADLSP 435
DB 358 QVENPNKEVAPYVSEAYNDEFEFSVLTGFTPGKFFYATNKKSSQVYCFNADLSP 417
QY 436 DSEDEGKTMTPTDFTTGKVKYTHIAGRDLFKYTVKPRDTPDPTFLKIKKVEIKGYREGK 494
DB 418 DYSQGETINPDSTIMEKAVYTHAGSDLFKVALRPDTPDEDFLKIKKVEIKGYREGK 477
QY 495 QAIYBSGLTETQARATQALAIYFTTSABELDKKLDYHGFQGMNDSTLAVALKILEY 550
DB 478 DS--YNGLTETQARATQALAIYFTTSADLTETKTYNNGKGYHGFESMDKKTALVVKELI 535
QY 551 EYADSNPQTLDTLDFEIPNNNKYQSLIGTQMPHEDLVDTIIRMEDK--EYIPVTNHLTLR 609
DB 536 TYAQNSAPQTLNDFEIPNNNSKDQSLIGTECHPDLDVDTIIRMEDKQEVIPVHSLTVK 595
QY 610 KTVYGLAGDRKDPHFETELKNNKOEILSQTVKTDKTNLEFKDKGATINLKHEBSLTLQ 669
DB 596 KTVYDELGDGKTGFQFETELKDKTGQIVYTLTNQDILVAKGKXSFNLKHDGDIRIEG 655
QY 670 LPBGYSTLVKRETSDEGKYKVNQSOEVANATVSKGITSDEFLAENNEPEVPTGVQDKI 729
DB 656 LPPTGYSTLKEAKKDVIVVQVSOEASGVSKDITEDKRVTFENKDLVPTGLTDDG 715
QY 730 NGYALIVAGISLGIW 746
DB 716 AITLWLLLVPLGLVW 732

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RESULT 3
US-10-282-122A-74295
; Sequence 74295, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELIPIRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848

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Query Match	5.7%	Score 223	DB 28	Length 770	
Best Local Similarity	21.0%	Pred. No. 8.6e-09			
Matches 158	Conservative 108	Mismatches 261		Indels 226	Gaps 39

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QY 649 EFKKQKATIN--LKRGESELTLOQLEPGSYLVKENDSGYV-----KVSQEVANVT 700
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 486 RDSGCK-TITWISIDGQVKDFYLMGKTFE-VEIAPDGEIVATAITFTVNEO--GOVTV 541
QY 701 SKGTGTSDETLAFENKKEPVPTG---VDOKI 729
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 542 NGKATKGDAHIVMDAVYKPTKGGSGVIDIEERL 574

RESULT 4
US-09-134-000-6122
: Sequence 6122, Application US/09134000A
: GENERAL INFORMATION:
: APPLICANT: Lynn Doucette-Stamm et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
: TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: GTC-005
: CURRENT APPLICATION NUMBER: US/09/134.000A
: CURRENT FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 6810
: SEQ ID NO 6122
: LENGTH: 1154
: TYPE: PRT
: ORGANISM: Enterococcus faecalis
US-09-134-000-6122

Query Match 5.2%; Score 205; DB 15; Length 1154;
Best Local Similarity 23.4%; Pred. No. 5.9e-07;
Matches 167; Conservative 85; Mismatches 231; Indels 230; Gaps 43;

QY 96 VNLEGS--RSYQVCFNLKKAFLPGSDSSVKKYKKHKGISTKFPD-----YAMSPRT 147
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 602 VSLGATINSSEIT-----LKGGEIHIQVR--IOTSENFKPDYQMGNTT 650
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 148 GDEINQKLRAYMNGHPQNGANGIMEGLPLNAIRVTOEAVVYSDNAPISNPDESFKRES 207
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 651 FQPLATAPEKVD-----GVPSGKAP--GVKLVKKIWEYDQDPTSPDNYIEIS 700
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 208 ESNLVST-----QLSLMQALKQLIDPLNATKMPQVDDQ--LSIFESEKDGKY 258
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 701 RKQYIVDANMVOGYIKLSKRPENDTSNSVERKNVTLQSTKADSEQVEVLGRLOYNNGQAF 760
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 259 NKGYONLLSGGLVPTKPPTPGDPMPRPQPTTSV--LIRKVAIGDSKLEGGATLQT 315
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 761 N--YQTPLELA-VREYSEKIDDTTKTKTKPKFPLDLKVINSSGE--KNLVAGVFLS 815
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 316 GDNVNSFCQARVSSND---IGRIELSDG--TYLTLELNSPAGYSIAEPITFKVEA--G 367
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 816 GKNV---QTLVDNKNKDGYSLPKDVRLQKGERYTLTEVKAPAGHGLAKTTWQIEVSBG 872
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 368 KVTITIDKQLENPKEKIVEPYSEAVYNDDEEFSV---LTTQ-----NNAKFIYA--K 415
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 873 KV--SIDQEVTTNQVI--PLEIE--NKFSSLPRIKKYTMQNGKQYNLAEEATFALQK 926
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 416 NKNSSQVYVCFNADLKSPDSESDGKTMTPDFTTGVEVKYTHIAGRLFFKYTVKPRDTP 475
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 927 NAGGSYQYVAIQKTD-----TTG----- 944
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 476 DTFLKHKIKVIEKG--YREKGOAIEYSGLETQLRAATOLAITYFTDSAEIDKDLKDYHG 534
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 945 ---LSYF-KISEPGEYR--MVEQSG---PLGVDYLAGUYEFT---VDK----- 980
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 535 FGDMMDSITLAVAKLIVEYAO---DSNPQLDLDFEIPNNKKNKQSLISTQMHHPEDLDII 591
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 981 YGR-----INAYGRNIENAEPM----- 999
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 592 RMEDKKEIVPTNHLTKR---TVTGLAGDRTKDFHFEILKNNKQELLSTQVTKDTKTL 648
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1000 -----LTHQNNLKPRLDVIYHKKADNQT-----PLKAGKFRILG-----PRDII 1037
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 649 EF-KDGKAT-----INLKHGE-SLTLOGLEPGYSYLVKETD---SEGKRVKVSQEVANA 698
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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QY	202	SEKREŠSNLVSTQSLSMRQALQOLDPNLT-----KMPKQVPDPFQ--LSI	248
Db	268	VTFEJORE---HTTNAAMKNGYIRIIKPAKQDTNTWERADIDIKLSHSGESYOEILSL	323
QY	249	FESEDKGDKNYNGYONLSSGLVPTKPPPG-----DPPMPBPNOQPTSV--LIRKXA	299
Db	324	POYNNQGAFFS--YQTI-----KELPPRGYDSQIDAMTKKTKQFPLPNLKITKNS	374
QY	300	IGDYSKLLLEGATLQTDGNVNSFOA-RVFSSNDIGERIEL-SDGYTTLTELNSPACYSIA	357
Db	375	TGE--KDLIGAVFKLTGDSIDPLTDHDGDTYSLEPNVAKLOEMFTYTLTEFKAPESGHS	432
QY	358	EPITFKVAGKYTI-IDGK-----QIENPKTIVEPYSVEALNDEEESVLT	405
Db	433	KRTWEIKIASDGYTLIDGKTIVTSDDTIQLTIENPFVSV--PVAIRKXAMQGTDEIML	490
QY	406	QNYAKFYAKNNKSSOYVVCENADLKSPPDSE---DGSKTMTDPDTTGEVKYTHTAGHD	462
Db	491	KGAFFSLQKKENGTYO-----PIDQOTNEKLASFDSLTPKRYRVEYTAGRA	539
QY	463	LFKYTVKPRDTPDTFLHKIKKVIIEKGYREKQGALEYSGLTETQLRAATQALAIYPTDSA	522
Db	540	GY-----DSPGNYERQIDKY-----GKII-YTGKNTMTNNVMTLTHQNRLLKAF	583
QY	523	ELDKDKLDYHGFQGMNDSTLAVAKILVEYADDSNPOLTDIDFPLPNNKIQSLIGTOM	582
Db	584	DLTVHKKED-----NGQTLKGAFFRLD-----GPEK-DLE-----	612
QY	583	HPEDIVDIIEMEDKKEVIVPTHNLRLKRVTVGLAGDRTPDFHEITELKNNQELLSQTVK	642
Db	613	SPKD-----GOETDTFLFE-----	626
QY	643	TDKTNLEFRKDGKATINLKHGE-SLTLOGLEPGYSYL--VKENDSEGYKVKNSQEVANA	698
Db	627	-----NLKPGYTLTLETFPBESYOGIKKEVTVLIYHEDSGIYQVDCQD--HE	669
QY	699	TVSKTGITSDE-TLAFENN-KEPVVPTGYDQKINGTALIVTAGISLGITW	746
Db	670	SVLSPGAKNNQISLIDITNQAKVPRLPETGTGIGRLGIY--LVGMIGCAFSIM	717
RESULT 8			
US-09-600-720-18			
; Sequence 18, Application US/09600720			
; GENERAL INFORMATION:			
; APPLICANT: GUSG, Bengt et al.			
; TITLE OF INVENTION: NOVEL FIBRONECTIN-BINDING PROTEIN			
; FILE REFERENCE: 0825-0161P			
; CURRENT APPLICATION NUMBER: US/09/600,720			
; CURRENT FILING DATE: 2000-09-20			
; NUMBER OF SEQ ID NOS: 18			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 18			
; LENGTH: 597			
; TYPE: PRT			
; ORGANISM: Streptococcus equi			
US-09-600-720-18			
Query Match 4.6%; Score 180; DB 20; Length 597;			
Best Local Similarity 20.8%; Pred. No. 2, 5e-05;			
Matches 149; Conservative 102; Mismatches 265; Indels 202; Gaps 34			
QY	68	SEYRWYGESVYR-GHPYKQFRVAVHDLRVNLGSGSYGYVCFNLKKAPPLSDSSVKTM	126
Db	32	AEQLLYGNNDGTRQSSPYF--LYVSPKNAAPKRELKDEYVYVCFNKKLIVPDOMESTIYSNF	89
QY	127	-----YKHDISTKFEDYAMSPRITQDELNQKLRVAVYNGHPONANGIMEG-	173
Db	90	NDIRSPYNDLPYEEKKLGIDGIFKQYAPDYKKDIDIASALVAALVNSNGYPTKMSQSLSTSY	149
QY	174	-LEPLNATRVQEAIVWYSDNAPJSPNPDSEKFRSEBSNVITSQLSLMQALKOLIDPNVL	232
Db	150	HLNNDSSKRYQLALAFYFSD-----SLTKLEYLMDTGGYVL-----NDMEKKALDFLLSKGE	200


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Db 176 ERHR-FDPKKLNTIKVGYGNLTTPSKNNNTYINHQADNKNKPPVPEYENIRFGYLELQ 234
Qy 148 GDELNOK-----LRVMTNGHQNANGIMEGLEPLN----- 178
Db 235 GSSLQKADTPNDKDRIPKPMPLIFHG--ENASSOLPSAGKENYGMNLYLSYDKRRP 292
Qy 179 AIRTOAAMVWYSSNAPISNPDESFKRESNLYTSQSLT----- 219
Db 293 ALSASDRVGYVYLNASGKSN-----EGDVVSAAHITVNGYQYKHTPATYOVDDPTN 343
Qy 220 -MROALKOLIDPLATKMPKOVDDF-----OLSFESSEDK--GDKYNGKYNOLSGG 269
Db 344 SLTGKLSYDNPNOQTQAGKYIKSQFDTKKVNETDYQIDAKINGNRFVGTASLVNEN 403
Qy 270 L-----VPTKPTPGDPPMPNPQOTTSVLIRKTAIGDYSKLBGATQLTGDNVNS 321
Db 404 TETAPFIKELESKKANPNP--NPN-----SPTLEGFYEGSGDEL-- 442
Qy 322 FOAFVSSND-----IGERIELSDGYTLTLELNSPAGYSIAEDPTFKVEAGKYVTTIDG 375
Db 443 --AGKFLSNDNASTVYVGKDKTDKPVAKTVFSAGFE--KPSTSFVDNETIGRLINS 498
Qy 376 KOIENPKKEIVE---PYSEAYNDF-----EEFSVLTTON-----YAKFYAK 415
Db 499 KKLMDAVNEKIDNDIDPTSDERIDEFPMGEKKAFFTKKVSSTQAVPAVFGQHDKIFY-- 556
Qy 416 NKNSSOVVYCFNADLKSPPDSEDEGKTMPDPTTGEV----- 453
Db 557 --NGNYVDLSASSVDKLAAPADAVKANOSIKEKYPNATLKNQVTAIVLQKAKNKPYYTA 614
Qy 454 ----KYTHIA-GRDLF-----KYTVKPRDTPDPTLKHKKVY----- 486
Db 615 IRAKSYHISGEFLYLDANOTPPRSTFVQGRADJSTTLTKAGKFTYNGIMAGYLIOKK 674
Qy 487 EKGREGQOAIIEYS---LTETOLRAATOLAIYFT-----DSAELEDKLDKDYHGF 535
Db 675 DKGYSNNEFIKKKHGDYLTED-----FTPEDDDDLASDSQDDAHGD 722
Qy 536 GDMMDSTLAVAKILVEYAQDSNPQTLDDDEFIPNNKYOSLIGTQMHPELDVIIRMED 595
Db 723 DDL-----IASDSQDDADAGDDSDDL--GDGADDAAGKYHAGN--IRPEF 767
Qy 596 KKEVIY---THNLT-----RKTYTGLAGDRTDHFETELKNNKQELL 637
Db 768 ENKLTLPNEPTHEKTFALDGNKNAKEDVDPTNSLTGLNDEKDIYFDI--KNGKIDGT 825
Qy 638 SQYVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETDSEGYKVKVNSQEVA- 696
Db 826 GFATAKADVPVRYREEVG---NNOGG-----GRLYNKIDLDVKGQFPGTNGEELAG 871
Qy 697 -----NATVSKTG 704
Db 872 QLOYDKGDGINDTAEKAG 889
```

RESULT 11
US-10-282-122A-62968
Sequence 62968, Application US/10282122A

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

```
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62968
LENGTH: 907
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-10-282-122A-62968
```

Query Match 4.5%; Score 177; DB 28; Length 907;
Best Local Similarity 20.6%; Pred. No. 9.4e-05;
Matches 164; Conservative 104; Mismatches 262; Indels 268; Gaps 40;

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Qy 84 YKQFRAVHADRLVNEGSRSYQVYCFNLKKA-----PPLGSDSSVKK-----YKKKHGCI 133
Db 165 YEDKFPKISDL--HLENSE-----HVFDAKKANNIKIYGYGLSSPAKPYMTYQOQONI 218
Qy 134 STR--FEDYA-----MSPRIT-----GDELNOKLRVMTNG--HPONANGIMEGL 174
Db 219 KKKRPGDYQNIIRGYMELRELNLKKKADQDSKNAIITFTPLFYGHNASHLP-- 276
Qy 175 EPLNAIRYTOAVWYTSNAP-----ISNPDE-----SKRESSESNLYTSQSLT----- 219
Db 277 --KAGKEDYEGNMLYLTLDVKKRPFLDKTDKVGTYFNSSTRKSNEGDLVSAHAITYLNSFK 333
Qy 220 -----MROALKOLIDPLATKMPKOVDDF-----OLSFESSEDK-- 254
Db 334 YKHTPATYVUPFDONTLKGKLSYDNPKNQJADGRTYSQDPTDKKVAEADYELDAKIN 393
Qy 255 GDKYNGKYNOLSGGL-----VPTKPTPGDPPMPNPQOTTSVLIRKTAIGDYSKL 306
Db 394 GNRFTGTAKSLIDNTNTAPFVKELFSKKANPNP--DPN-----SDT 434
Qy 307 LEGATTLQITGDNVNSFOARVSSNDI-----GERIELSDGYTLTLELNSPAGYSIAEP 359
Db 435 LEGGFYEGSGDEL--AGKFLSNDNATFVVEGKDKRKTDPVAKTVFYS--TGFE--KP 487
Qy 360 ITFKVEAGKYVTTIDGK-----QIENPNKEIPEYSEAYNDF-----EEFSVLT 405
Db 488 STSFVGNELGISIIDGKLNDEVNNOJEDERIVPNSKKEYIENYGRPKQKTKKIMASVO 547
Qy 406 QNYA-----KFYV-----AK--NKNSSOVVYCFNADLKSPPDSEDEGKTMPDPT 449
Db 548 KNPAYFGQHDKIFYNGNYYDLSAKKANLIGVSQDTSKSLAKYPPDA--KYSTDKV 603
Qy 450 T-----GVTYKTHIAGRLKFLKTYKPRDPTDPTLTK----- 480
Db 604 TKIVLOQAKDPYTAHAKSYDHSIFGVLVNDNKGNTFRSYFVQGGQADVSTQLPSAGK 663
Qy 481 -----HIKKVIEKGYREKGOAIEYSGLTQLRAATOLAIYFT-----DSAE 524
```

Db 664 FTYNGMAGYLQKKKGYSKDEDTIKOKGLKD-----YLTQKFIPODDDDDD 712
QY 525 DMDKL-----KOHFGDMNDSTLAAKILVEYAODSNRPOLDLDFEIRNNKKYQS 576
Db 713 DDDSLASDSDSDNNHGDGDDL-----IASDSDSDDDADGDDSDDL--GDDADDD 761
QY 577 LIGTQHPEDLVDLIIMEDKKEVIVP---THNLTL-----RKTVTGLAGD 618
Db 762 AGKVVHAGN---IRPEENKYLPINEPTHEKTFALDGNKAKAFDVNPTNSLTGKLAND 817
QY 619 RIKDFHEIELEKNNKQELLSQLVTKDTNLEFKDGKATINLKHGESLTLQGLPEGYSYLV 678
Db 818 ERDDIYFDI--KNGKIDGTGTAKADVPVNYREEVG---NNQCG-----GFLYNI 861
QY 679 KETDSEGYKVVNSOEVA 696
Db 862 KDIDVKGQFFGTNGEELA 879

RESULT 12

US-09-445-096a-70
; Sequence 70, Application US/09445096A
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Quljun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; FILE REFERENCE: 1038-989 MIS
; CURRENT APPLICATION NUMBER: US/09/445, 096A
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 08/867, 941
; PRIOR FILING DATE: 1997-06-03
; PRIOR APPLICATION NUMBER: PCT/CA98/00544
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 905
; TYPE: PRN
; ORGANISM: Moraxella catarrhalis
US-09-445-096a-70

Query Match 4.5%; Score 176; DB 18; Length 905;
Best Local Similarity 20.6%; Pred. No. 0.00011;
Matches 164; Conservative 102; Mismatches 264; Indels 266; Gaps 40;

QY 84 YKQFVAVHDLRYNLEGSRSYQVYCFNLKKA-----FPLGSDSSVKK-----WYKKHDCI 133
Db 165 YEDKPFKISDL--HLENSE-----HYVDKAKANNIKIYIGALLSPAKNPTMYNQDEQNT 218
QY 134 STR--FEDYA-----MSPRIT-----GDELNOKIRAVMYNG-----HPQANGIMEGI 174
Db 219 KKKKPPDDQONIRFGYMELELDLNNKQSDKKRAIIFTPTLFHYGENASTHLP-- 276
QY 175 EPLNARIVQEAQVWYSDAP-----ISNDE-----SFKRSESNLYSTLSL-- 219
Db 277 ---KAKFDYEGNWLTLTVKKRPFLDKTDKGVYFNSTRKSNEDLVSAHIYNSFK 333
QY 220 -----MROALKOLIDPNLATKMPKQVPDDE-----OLSIPESEDK-- 254
Db 334 YKHTPATYVSDPDQNTLKGKLSYDNPKNQOTADGRITRSQFDTKDVKNENADYETDAKIN 393
QY 255 GKYNKGYONLSGLG-----VPTKPPDPPMPPPNOQUTSVLIRKAIAGDYSKU 306
Db 394 GKRFTGTAJSLIDNTNTAPVYKELFSKKNPNP--DPN-----SDT 434
QY 307 LEGATLQLTGDNVNSQAVVSSNDI-----GERIELSDGTYTLTLEINSFAGYSIAEP 359
Db 435 LEEGFGESGDEL---AGKFLSNDNATEVVEFGKRDKTEEPVATKYVFS--TGFE--KP 487

QY 360 IFEKVEAGVYTLIIDK---QIENPNKEIVESVYEAYNDF-----EESVLT 405
Db 488 STSFVGNELIGSLIDKGLNDEVNNOLEDETIVNSKEYEYVGNPNQFTKKIANSG 547
QY 406 QNTA-----KEYY-----AK--NKGSSOVYVCFNADLKSPPDSEDCGKTMPDT 449
Db 548 KNPAYFGOHDKKEFYFNQNYDLISAKKANKLGVSODTSTNKSLAKYPDA---KVSIDNKV 603
QY 450 T-----GEVYTHIARQDLFKYTVKRDIDPPTEFK----- 480
Db 604 TKIVLOQAKDPYTAIIHANSYDHSIFGEVLYNDNKNPNRSTFVGQGVADVSTQLPSAK 663
QY 481 -----HIKVEIKGYREKGALEYGLTETOLRAATOLAIYFT----- 519
Db 664 FTYNGMAGYLQKKKGYSKDEDTIKOKGLKD-----YLTQKFIPODDDDDD 712
QY 520 DSAEILDKKIKD--YHFGDMNDSTLAAKILVEYAODSNRPOLDLDFEIRNNKKYQSLI 578
Db 713 DSLTASDSDSDNNHGDGDDL-----IASDSDSDDDDDGDDSDDL--GDDADDDAA 761
QY 579 GTQWHEEDLVDLIIMEDKKEVIVP---THNLTL-----RKTVTGLAGDRT 620
Db 762 GKYYHAGN---IRPEENKYLPINEPTHEKTFALDGNKAKAFDVNPTNSLTGKLAND 817
QY 621 KDFHEIELEKNNKQELLSQLVTKDTNLEFKDGKATINLKHGESLTLQGLPEGYSYLV 680
Db 818 GDIVFDI--KNGKIDGTGTAKADVPVNYREEVG---NNQCG-----GFLYNI 861
QY 681 TDESGYKVVNSOEVA 696
Db 862 IDVKGRFFGTNGEELA 879

RESULT 13

US-09-134-000-4971
; Sequence 4971, Application US/09134000A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
; TITLE OF INVENTION: PARACALS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-005
; CURRENT APPLICATION NUMBER: US/09/134, 000A
; CURRENT FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 6810
; SEQ ID NO 4971
; LENGTH: 1233
; TYPE: PRN
; ORGANISM: Enterococcus faecalis
US-09-134-000-4971

Query Match 4.3%; Score 168; DB 15; Length 1233;
Best Local Similarity 21.5%; Pred. No. 0.00093;
Matches 163; Conservative 105; Mismatches 323; Indels 168; Gaps 42;

QY 39 ALVTSNAGKATVGLVES---STPNAINPDSSSEYRWYGVESYVGRPHYKOFRYAHLR 95
Db 515 SLSTPIYIGPNKAIQVSDQYIEISVYN--LNAETAMGNYDQ-----NGAYSSR 562
QY 96 ---VNEGSRSYQVYCFNLKKAEP-----LQSDSSVKKWYKKHGDISKFEEDYAMSPRITD 149
Db 563 TVVSVMSKREKPIQNLRIKHPNYLSLRATKEIYYK---LGT---DYVTTPSDDS 615
QY 150 ELNOKIRAVMYNGHPQANGIMEGL-----PLNARIVQEAQVWYSDAPISNPDESFK 204
Db 616 VIKFTPTTNEIQIPIGFNYVPDLSLKDKSIPVDITPTMSAEGLTVPDVTYTT--NSK 672
QY 205 RESESNLYSTLSLIRQALKOLIDPNLATKMPKQVPDFOQLSIFESSEDCGKYNKGYON 264
Db 673 RGSERLQSSKNOFLVNAANDSFDSLSTVTKTPAGA--DYLDIYVSN--DOVDSIYQ 728
QY 265 LLSGLVPTKPPPTPGDPPMP--PNOPQUTSVL-----RKYAIGDYSKL---LEGATLQ 313
Db 729 YMDRGQYFDKPMTPNPSGYPTITFDENTNSYTFDFGKTAKRYII--EYKANANGMIDVPTLY 787

QY 314 LAG-----DYNFQARVSSNDIGERIELSDGTYTLTLEINSPAGYSIAEPITTFKEVAG 367
DB 788 ITGTAKPEOSNNNEGASVYON---EALDILSAT-----QANPLTKNVYTT 832
QY 368 KYVT-IIDGK--QIENPNKEIPEYSEVAYNDFEESVLTTONYAKFYAKNKGSSQYV 424
DB 833 YVTTKNIDKHTHRVKNPTELTLPKGTNNQIDLNSTTV-----KVPEDA 877
QY 425 YCFNADLKSPDSEGGKMTDPFTTGE---VKYTHIARDLFKYTVKPRDPTFLKH 481
DB 878 Y-----SLEKTNAGAKVIFKDYLTLENTITIEYNTVSANAGIYETITIDSETLQMSA 930
QY 482 IKKVI-----EKGYREKQALIEYSGLTFTOLRAATQALAYFTD---SABL 524
DB 931 SKKVTYTABITLKFSEGAEGIYLTATFTYHNVEDENQALAKVSFELIDNVTHTATEF 990
QY 525 DKDKLDYHGFQDM-NDSTLAVAKILVEYAODSNPOLT-----DLDFEIP----- 569
DB 991 TDEKQYGFDAIMTGDYTLRTNVPOEYSDBE--YLTGKAIKLVKGNOLKIPLTXTI 1048
QY 570 NNNKTYO-----SLGTQWHPEDLVDIIRMEDK-EVYPTNHLTKTYTGLAGDKTDF 623
DB 1049 DHSRLQVKDSTIYVGSMPKEE--NFVSATDKTGQDVPE-----KITVSGOV-DNFTKAG 1100
QY 624 HEIELKN-NKOELLQYTKTDTKTNLEFKDGKATINLKHGESITLQGLEGSYLVKED 682
DB 1101 VPIIYSDGKETATVYTKPQOSKLEVND--TTIYV--GDSMK-----PE--DNFVSATD 1150
QY 683 SEGKYV--KVSQEVANATVSKGTITSDETLAFENKKE 718
DB 1151 KTGQDVPEKIDVQGTVN--VDKIG--DYELIYKNGKK 1184

RESULT 14
US-09-134-000C-4971
; Sequence 4971, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4971
; LENGTH: 1233
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4971

Query Match 4.3%; Score 168; DB 15; Length 1233;
Best local Similarity 21.5%; Pred. No. 0.00093;
Matches 163; Conservative 105; Mismatches 323; Indels 168; Gaps 42;

QY 39 ALVTSNMGAKTYFGLVES---STPNAINDSSSEYRWYGESYVRGHPYKQFRVAHDLR 95
DB 515 SLSTPIGPNKAIQLVSDQYIEPISVNP-LNAETAMGNVDDQ-----NGAYSSR 562
QY 96 --VNEGSRSYOYVCNKLKAP-----LGSDSYKWKYKKGKIGISTKFEDYAMSPTITD 149
DB 563 TTVSVGSKKEQIONLEIKVHPNLSLRATKEIFYYK---LGT---DYVTPTSDS 615
QY 150 ELNOKLRAMVNGHPNANGIMEGLE-----PLNATRYQEAUVWYSDNAPISNDESPK 204
DB 616 VIKFTPTITNEIQIPIGFNYVPDSLPKKDSIPVDITPITMSABGLTPUTTYTT---NKK 672
QY 205 RESESNLVSTQSLIMRQALKOLIDPNLATKMPKQVDDFOLSTFESEDKGKYNKGYON 264
DB 673 RRSERTIGSSKNQFLVNAHNSFDSLSTVKTIPAGA--DVLPDIYDVSN--DQVDSITYQ 728

QY 265 LLSGLVPTKPPPTPGDPPMP--PNQPTTSVL-----RKXAGIDSKL---LEGATQ 313
DB 729 YMDRGQYFDKPMTPNSPGYPTTFEDENTSYTFDEGKTKRYII-EYKNANGMIDVPTLY 787
QY 314 LAG-----DYNFQARVSSNDIGERIELSDGTYTLTLEINSPAGYSIAEPITTFKEVAG 367
DB 788 ITGTAKPEOSNNNEGASVYON---EALDILSAT-----QANPLTKNVYTT 832
QY 368 KYVT-IIDGK--QIENPNKEIPEYSEVAYNDFEESVLTTONYAKFYAKNKGSSQYV 424
DB 833 YVTTKNIDKHTHRVKNPTELTLPKGTNNQIDLNSTTV-----KVPEDA 877
QY 425 YCFNADLKSPDSEGGKMTDPFTTGE---VKYTHIARDLFKYTVKPRDPTFLKH 481
DB 878 Y-----SLEKTNAGAKVIFKDYLTLENTITIEYNTVSANAGIYETITIDSETLQMSA 930
QY 482 IKKVI-----EKGYREKQALIEYSGLTFTOLRAATQALAYFTD---SABL 524
DB 931 SKKVTYTABITLKFSEGAEGIYLTATFTYHNVEDENQALAKVSFELIDNVTHTATEF 990
QY 525 DKDKLDYHGFQDM-NDSTLAVAKILVEYAODSNPOLT-----DLDFEIP----- 569
DB 991 TDEKQYGFDAIMTGDYTLRTNVPOEYSDBE--YLTGKAIKLVKGNOLKIPLTXTI 1048
QY 570 NNNKTYO-----SLGTQWHPEDLVDIIRMEDK-EVYPTNHLTKTYTGLAGDKTDF 623
DB 1049 DHSRLQVKDSTIYVGSMPKEE--NFVSATDKTGQDVPE-----KITVSGOV-DNFTKAG 1100
QY 624 HEIELKN-NKOELLQYTKTDTKTNLEFKDGKATINLKHGESITLQGLEGSYLVKED 682
DB 1101 VPIIYSDGKETATVYTKPQOSKLEVND--TTIYV--GDSMK-----PE--DNFVSATD 1150
QY 683 SEGKYV--KVSQEVANATVSKGTITSDETLAFENKKE 718
DB 1151 KTGQDVPEKIDVQGTVN--VDKIG--DYELIYKNGKK 1184

RESULT 15
US-10-434-665-4971
; Sequence 4971, Application US/10434665
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PAT03-09
; CURRENT APPLICATION NUMBER: US/10/434,665
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 09/134,000
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4971
; LENGTH: 1233
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-434-665-4971

Query Match 4.3%; Score 168; DB 30; Length 1233;
Best local Similarity 21.5%; Pred. No. 0.00093;
Matches 163; Conservative 105; Mismatches 323; Indels 168; Gaps 42;

QY 39 ALVTSNMGAKTYFGLVES---STPNAINDSSSEYRWYGESYVRGHPYKQFRVAHDLR 95
DB 515 SLSTPIGPNKAIQLVSDQYIEPISVNP-LNAETAMGNVDDQ-----NGAYSSR 562
QY 96 --VNEGSRSYOYVCNKLKAP-----LGSDSYKWKYKKGKIGISTKFEDYAMSPTITD 149
DB 563 TTVSVGSKKEQIONLEIKVHPNLSLRATKEIFYYK---LGT---DYVTPTSDS 615
QY 150 ELNOKLRAMVNGHPNANGIMEGLE-----PLNATRYQEAUVWYSDNAPISNDESPK 204

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Db 616 VIKFTPTNEIQIPGFNVYVPSLIPKDKSIPVDIPIPTMSAEGILPVDITVT---NSK 672
QY 205 RESESNLVSTQSOLMROALKQLIDPNLATFKMPKOVDPDDFQLSIESEDKGDKYKNGYQN 264
Db 673 RGSERITQSSKNOGLVARNDSFDSLYRKIPAGA--DVLFDIYDSN--DOYDSITPQ 728
QY 265 LLSGGLVPTKPPPPGDDPMP--PNQPTTSVLI-----RKYAGDYSKL---LEGATLQ 313
Db 729 YMDRGQYFDKPMTPNSGYPTITFDEMTNSYTFDFGKTNKRYII-EYKNANGWIDVPTLY 787
QY 314 LTG-----DNVNFQARFVSSNDIGERIELSDGTITTELNSPAGYSIAEPTIFKYBAG 367
Db 788 ITGTAKEPQSNNEGSAVSQN---EALDILSAT-----QAANPTLKNYTKT 832
QY 368 KVVY-IIDGK--QIENPNKEIVEPYSVYEAANDFEFVSULTQNYAKFPYAKNKNSSQYV 424
Db 833 TVTTKNIDNKNHRYKNPTIELTPKGTINAQIDLNSTV-----KVPEDA 877
QY 425 YCFNADLKSPDSEDGKMTDPFTTGE--VKYTHIAGRDLFKYTVKPRDTPDPTFLKH 481
Db 878 Y-----SLEKTINGAKVIFKDYTLTENITIEYNTVSANNGQIYTETTIDSETLNQMSA 930
QY 482 IKKYI-----EKGYREKGAIEYSGLETQLRATQLAIFYFTD---SAEL 524
Db 931 SKKKVTTAPITLKESEGDAGEIYVYATATFYNHVEDENQAIKVSFELIDNVHTATF 990
QY 525 DKOKLKDYHGFQDM-NDSTLAVAKILVEYADDSNPQOLT-----DLDFTP----- 569
Db 991 TTDEKGOYSFDALMTGDTTLKVTNVPQOYSYDEE--YLTGKAIKLVKGDNOQLIPTKTI 1048
QY 570 NNNKYQ-----SLIGTQWHPEDLVDIRMEDKK-EVIPVTHNLTLRKVTGLAGDRTKDF 623
Db 1049 DHSRLQYKDSITIVYGD SMKPEE--NFVSATDKTGQDVPE-----KITVSGQV-DNTRKAG 1100
QY 624 HFEIETLKN-NKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLOGLPEGYSYLKVED 682
Db 1101 VYPIYSDEGKEETAYTVKPDOSKLEVKD--TIIYV--GDSWK-----PE--DNFVSATD 1150
QY 683 SEGKYV---KVNQOEVANATVSKGITSDETLAFENKKE 718
Db 1151 KTGQDVPEFKIDVQGTYN--VDKITG---DYEIYVKNNGK 1184
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Search completed: August 19, 2003, 15:28:27
Job time : 294 secs